

# Sequence Listing

<110> de Sauvage, Frederic J.  
Gurney, Austin  
Murone, Maximilien  
Rosenthal, Arnon  
Stone, Donna M.  
Wood, William I.

<120> Human Suppressor of Fused

<130> P1548R1-US

<150> US 60/123,090

<151> 1999-03-05

<150> US 60/135,736

<151> 1999-05-25

<150> PCT/US00/05746

<151> 2000-03-02

<160> 10

<210> 1

<211> 1760

<212> DNA

<213> Homo sapiens

<400> 1

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cagtgcctgc cctacgcacc ccgatggcgg agctgcggcc tagcggcgcc 100  
cccgccccca ccgcgcccc ggccectggc ccgaactgcc ccccgccctt 150  
cgcttcgctc tttcccccg gactgcacgc catctacgga gagtgccgcc 200  
gcctttaccc tgaccagccg aaccgcgtcc aggttacgc tatcgtcaag 250  
tactggttgg gtggcccaga ccccttggaac tatgttagca tgtacaggaa 300  
tgtgggggagc cttctgcta acatccccga gcaactggac tacatcagct 350  
tcggcctgag tgatctctat ggtgacaaca gagtccatga gtttacagga 400  
acagatggac ctagtggttt tggctttgag ttgacctttc gtctgaagag 450  
agaaactggg gagtctgccc caccaacatg gcccgagag ttaatgcagg 500  
gcttggcacg atacgtgttc cagtcagaga acaccttctg cagtggggac 550  
catgtgtcct ggcacagccc tttggataac agtgagtcaa gaattcagca 600  
catgctgctg acagaggacc cacagatgca gcccgtcag acacccttg 650  
gggtagttac cttctccag atcgttggtg tctgcaactga agagctacac 700  
tcagcccagc agtggaaagg gcagggcatc ctggagctgc tgcggacagt 750  
gcctattgct ggcgggccct ggctgataac tgacatgcgg aggggagaga 800

ccatatttga gatcgatcca cacctgcaag agagagttga caaaggcatc 850  
gagacagatg gctccaacct gagtggtgtc agtgccaagt gtgcctggga 900  
tgacctgagc cggccccccg aggatgacga ggacagccgg agcatctgca 950  
tcggcacaca gccccggcga ctctctggca aagacacaga gcagatccgg 1000  
gagaccctga ggagaggact cgagatcaac agcaaacctg tccttccacc 1050  
aatcaacctt cagcggcaga atggcctcgc ccacgaccgg gccccgagcc 1100  
gcaaagacag cctggaaagt gacagctcca cggccatcat tccccatgag 1150  
ctgattcgca cgcggcagct tgagagcgta catctgaaat tcaaccagga 1200  
gtccggagcc ctcatctc tctgcctaag gggcaggctc ctgcatggac 1250  
ggcactttac atataaaaagt atcacaggtg acatggccat cacgtttgtc 1300  
tccacgggag tggaaggcgc ctttgccact gaggagcatc cttacgcggc 1350  
tcatggaccc tggttacaac tctgaacctt tcctcggagc tctgccctcc 1400  
cgtcctggaa cgtctttctg ccctgaggag agggtagtca gcattctcaa 1450  
ttttcagcag ctcaagaacc ttggccccc aaggacttcg cagatgtcac 1500  
attgcccctc agtcccctga atgcccttcg gacccaaccc caattcccc 1550  
agcccctgac cccctagctg ccgggggttc cactcccagt gccacaaccc 1600  
cctcacctcc cctggcagcc cctcagcgag cctgaggccc agcaccogct 1650  
ggctccccag cacatggtcc cctcccatgg gctgttgccc agggaaccgg 1700  
ggcgcggtgg gaacgagctg ctggcctcgg catgtttcaa taaagttgct 1750  
gtgctgggag 1760

<210> 2  
<211> 431  
<212> PRT  
<213> Homo sapiens

<400> 2  
Met Ala Glu Leu Arg Pro Ser Gly Ala Pro Gly Pro Thr Ala Pro  
1 5 10 15  
Pro Ala Pro Gly Pro Thr Ala Pro Pro Ala Phe Ala Ser Leu Phe  
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Pro Pro Gly Leu His Ala Ile Tyr Gly Glu Cys Arg Arg Leu Tyr  
35 40 45  
Pro Asp Gln Pro Asn Pro Leu Gln Val Thr Ala Ile Val Lys Tyr  
50 55 60  
Trp Leu Gly Gly Pro Asp Pro Leu Asp Tyr Val Ser Met Tyr Arg  
65 70 75

Asn Val Gly Ser Pro Ser Ala Asn Ile Pro Glu His Trp His Tyr  
 80 85 90  
 Ile Ser Phe Gly Leu Ser Asp Leu Tyr Gly Asp Asn Arg Val His  
 95 100 105  
 Glu Phe Thr Gly Thr Asp Gly Pro Ser Gly Phe Gly Phe Glu Leu  
 110 115 120  
 Thr Phe Arg Leu Lys Arg Glu Thr Gly Glu Ser Ala Pro Pro Thr  
 125 130 135  
 Trp Pro Ala Glu Leu Met Gln Gly Leu Ala Arg Tyr Val Phe Gln  
 140 145 150  
 Ser Glu Asn Thr Phe Cys Ser Gly Asp His Val Ser Trp His Ser  
 155 160 165  
 Pro Leu Asp Asn Ser Glu Ser Arg Ile Gln His Met Leu Leu Thr  
 170 175 180  
 Glu Asp Pro Gln Met Gln Pro Val Gln Thr Pro Phe Gly Val Val  
 185 190 195  
 Thr Phe Leu Gln Ile Val Gly Val Cys Thr Glu Glu Leu His Ser  
 200 205 210  
 Ala Gln Gln Trp Asn Gly Gln Gly Ile Leu Glu Leu Leu Arg Thr  
 215 220 225  
 Val Pro Ile Ala Gly Gly Pro Trp Leu Ile Thr Asp Met Arg Arg  
 230 235 240  
 Gly Glu Thr Ile Phe Glu Ile Asp Pro His Leu Gln Glu Arg Val  
 245 250 255  
 Asp Lys Gly Ile Glu Thr Asp Gly Ser Asn Leu Ser Gly Val Ser  
 260 265 270  
 Ala Lys Cys Ala Trp Asp Asp Leu Ser Arg Pro Pro Glu Asp Asp  
 275 280 285  
 Glu Asp Ser Arg Ser Ile Cys Ile Gly Thr Gln Pro Arg Arg Leu  
 290 295 300  
 Ser Gly Lys Asp Thr Glu Gln Ile Arg Glu Thr Leu Arg Arg Gly  
 305 310 315  
 Leu Glu Ile Asn Ser Lys Pro Val Leu Pro Pro Ile Asn Pro Gln  
 320 325 330  
 Arg Gln Asn Gly Leu Ala His Asp Arg Ala Pro Ser Arg Lys Asp  
 335 340 345  
 Ser Leu Glu Ser Asp Ser Ser Thr Ala Ile Ile Pro His Glu Leu  
 350 355 360  
 Ile Arg Thr Arg Gln Leu Glu Ser Val His Leu Lys Phe Asn Gln  
 365 370 375

Glu Ser Gly Ala Leu Ile Pro Leu Cys Leu Arg Gly Arg Leu Leu  
 380 385 390

His Gly Arg His Phe Thr Tyr Lys Ser Ile Thr Gly Asp Met Ala  
 395 400 405

Ile Thr Phe Val Ser Thr Gly Val Glu Gly Ala Phe Ala Thr Glu  
 410 415 420

Glu His Pro Tyr Ala Ala His Gly Pro Trp Leu  
 425 430

<210> 3  
 <211> 346  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> consensus DNA used to isolate DNA 33454

<220>  
 <221> unsure  
 <222> 8, 28, 39, 54-55, 65, 68, 74, 80, 90, 125, 130  
 <223> unknown base

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 gccnnaactgc cccnccgnc ttancatctn tctttcccan gggactgcac 100  
 gccatctacg gagagtgccg ccgcntttan ccttaccagc cgaacccgct 150  
 ccagggttacc gctatcgtca agtactgggt ggggtggccca gaccccttgg 200  
 actatggttag catgtacagg aatgtgggga gcccttctgc taacatcccc 250  
 gagcactggc actacatcag cttcggcctg agtgatctct atggtgacaa 300  
 cagagtccat gaagtttaca ggaacagatg gacctagtgg ttttgt 346

<210> 4  
 <211> 468  
 <212> PRT  
 <213> Drosophila Melanogaster

<400> 4  
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Pro Gly Leu Lys Ala Ile Ile Asp His Leu Gly Gln Val Tyr Pro  
 20 25 30

Asn Gln Pro Asn Pro Leu Gln Val Thr Thr Leu Leu Lys Tyr Trp  
 35 40 45

Leu Gly Gly Gln Asp Pro Leu Asp Tyr Ile Ser Met Tyr Lys Phe  
 50 55 60

Pro Gly Asp Val Asp Arg Asn Val Pro Pro His Trp His Tyr Ile  
 65 70 75

Ser Phe Gly Leu Ser Asp Leu His Gly Asp Glu Arg Val His Leu  
 80 85 90  
 Arg Glu Glu Gly Val Thr Arg Ser Gly Met Gly Phe Glu Leu Thr  
 95 100 105  
 Phe Arg Leu Ala Lys Thr Glu Ile Glu Leu Lys Gln Gln Ile Glu  
 110 115 120  
 Asn Pro Glu Lys Pro Gln Arg Ala Pro Thr Trp Pro Ala Asn Leu  
 125 130 135  
 Leu Gln Ala Ile Gly Arg Tyr Cys Phe Gln Thr Gly Asn Gly Leu  
 140 145 150  
 Cys Phe Gly Asp Asn Ile Pro Trp Arg Lys Ser Leu Asp Gly Ser  
 155 160 165  
 Thr Thr Ser Lys Leu Gln Asn Leu Leu Val Ala Gln Asp Pro Gln  
 170 175 180  
 Leu Gly Cys Ile Asp Thr Pro Thr Gly Thr Val Asp Phe Cys Gln  
 185 190 195  
 Ile Val Gly Val Phe Asp Asp Glu Leu Glu Gln Ala Ser Arg Trp  
 200 205 210  
 Asn Gly Arg Gly Val Leu Asn Phe Leu Arg Gln Asp Met Gln Thr  
 215 220 225  
 Gly Gly Asp Trp Leu Val Thr Asn Met Asp Arg Gln Met Ser Val  
 230 235 240  
 Phe Glu Leu Phe Pro Glu Thr Leu Leu Asn Leu Gln Asp Asp Leu  
 245 250 255  
 Glu Lys Gln Gly Ser Asp Leu Ala Gly Val Asn Ala Asp Phe Ser  
 260 265 270  
 Phe Arg Glu Leu Lys Pro Thr Lys Glu Val Lys Glu Glu Val Asp  
 275 280 285  
 Phe Gln Ala Leu Ser Glu Lys Cys Ala Asn Asp Glu Asn Asn Arg  
 290 295 300  
 Gln Leu Thr Asp Thr Gln Met Lys Arg Glu Glu Pro Ser Phe Pro  
 305 310 315  
 Gln Ser Met Ser Met Ser Ser Asn Ser Leu His Lys Ser Cys Pro  
 320 325 330  
 Leu Asp Phe Gln Ala Gln Ala Pro Asn Cys Ile Ser Leu Asp Gly  
 335 340 345  
 Ile Glu Ile Thr Leu Ala Pro Gly Val Ala Lys Tyr Leu Leu Leu  
 350 355 360  
 Ala Ile Lys Asp Arg Ile Arg His Gly Arg His Phe Thr Phe Lys  
 365 370 375  
 Ala Gln His Leu Ala Leu Thr Leu Val Ala Glu Ser Val Thr Gly

	380		385		390
Ser Ala Val Thr	Val Asn Glu Pro Tyr	Gly Val Leu Gly Tyr Trp			
	395	400		405	
Ile Gln Val Leu	Ile Pro Asp Glu Leu	Val Pro Arg Leu Met Glu			
	410	415		420	
Asp Phe Cys Ser	Ala Gly Leu Asp Glu	Lys Cys Glu Pro Lys Glu			
	425	430		435	
Arg Leu Glu Leu	Glu Trp Pro Asp Lys	Asn Leu Lys Leu Ile Ile			
	440	445		450	
Asp Gln Pro Glu	Pro Val Leu Pro Met	Ser Leu Asp Ala Ala Pro			
	455	460		465	
Leu Lys Met					

<210> 5  
 <211> 275  
 <212> DNA  
 <213> Mus musculus

<400> 5  
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 gctatcg tca agtactgggtt ggggtgg tccg gaccccttgg actatg ttag 100  
 catgtacagg aacatgg gga gtccttctgc caacatccct gagcactggc 150  
 actacatcag ctttggcctg agtgatctct atgggtgacaa cagagtccat 200  
 gagtttacag gaacagacgg accaagtgga tttggctttg agttgacgtt 250  
 tcgtctgaag agagaaactg gggag 275

<210> 6  
 <211> 23  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> forward PCR cloning primer

<400> 6  
 cagccgaacc cgctccaggt tac 23

<210> 7  
 <211> 25  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> reverse PCR cloning primer

<400> 7  
 catggactct gttgtcacca tagag 25

<210> 8

<211> 40  
<212> DNA  
<213> Artificial sequence

<220>  
<223> hybridization probe

<400> 8  
gagcactggc actacatcag ctttggcctg agtgatctct 40

<210> 9  
<211> 441  
<212> PRT  
<213> Artificial sequence

<220>  
<223> hSu(fu) epitope flag protein

<400> 9  
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Pro Ala Pro Gly Pro Thr Ala Pro Pro Ala Phe Ala Ser Leu Phe  
20 25 30  
Pro Pro Gly Leu His Ala Ile Tyr Gly Glu Cys Arg Arg Leu Tyr  
35 40 45  
Pro Asp Gln Pro Asn Pro Leu Gln Val Thr Ala Ile Val Lys Tyr  
50 55 60  
Trp Leu Gly Gly Pro Asp Pro Leu Asp Tyr Val Ser Met Tyr Arg  
65 70 75  
Asn Val Gly Ser Pro Ser Ala Asn Ile Pro Glu His Trp His Tyr  
80 85 90  
Ile Ser Phe Gly Leu Ser Asp Leu Tyr Gly Asp Asn Arg Val His  
95 100 105  
Glu Phe Thr Gly Thr Asp Gly Pro Ser Gly Phe Gly Phe Glu Leu  
110 115 120  
Thr Phe Arg Leu Lys Arg Glu Thr Gly Glu Ser Ala Pro Pro Thr  
125 130 135  
Trp Pro Ala Glu Leu Met Gln Gly Leu Ala Arg Tyr Val Phe Gln  
140 145 150  
Ser Glu Asn Thr Phe Cys Ser Gly Asp His Val Ser Trp His Ser  
155 160 165  
Pro Leu Asp Asn Ser Glu Ser Arg Ile Gln His Met Leu Leu Thr  
170 175 180  
Glu Asp Pro Gln Met Gln Pro Val Gln Thr Pro Phe Gly Val Val  
185 190 195  
Thr Phe Leu Gln Ile Val Gly Val Cys Thr Glu Glu Leu His Ser  
200 205 210

Ala Gln Gln Trp Asn Gly Gln Gly Ile Leu Glu Leu Leu Arg Thr  
 215 220 225  
 Val Pro Ile Ala Gly Gly Pro Trp Leu Ile Thr Asp Met Arg Arg  
 230 235 240  
 Gly Glu Thr Ile Phe Glu Ile Asp Pro His Leu Gln Glu Arg Val  
 245 250 255  
 Asp Lys Gly Ile Glu Thr Asp Gly Ser Asn Leu Ser Gly Val Ser  
 260 265 270  
 Ala Lys Cys Ala Trp Asp Asp Leu Ser Arg Pro Pro Glu Asp Asp  
 275 280 285  
 Glu Asp Ser Arg Ser Ile Cys Ile Gly Thr Gln Pro Arg Arg Leu  
 290 295 300  
 Ser Gly Lys Asp Thr Glu Gln Ile Arg Glu Thr Leu Arg Arg Gly  
 305 310 315  
 Leu Glu Ile Asn Ser Lys Pro Val Leu Pro Pro Ile Asn Pro Gln  
 320 325 330  
 Arg Gln Asn Gly Leu Ala His Asp Arg Ala Pro Ser Arg Lys Asp  
 335 340 345  
 Ser Leu Glu Ser Asp Ser Ser Thr Ala Ile Ile Pro His Glu Leu  
 350 355 360  
 Ile Arg Thr Arg Gln Leu Glu Ser Val His Leu Lys Phe Asn Gln  
 365 370 375  
 Glu Ser Gly Ala Leu Ile Pro Leu Cys Leu Arg Gly Arg Leu Leu  
 380 385 390  
 His Gly Arg His Phe Thr Tyr Lys Ser Ile Thr Gly Asp Met Ala  
 395 400 405  
 Ile Thr Phe Val Ser Thr Gly Val Glu Gly Ala Phe Ala Thr Glu  
 410 415 420  
 Glu His Pro Tyr Ala Ala His Gly Pro Trp Leu Gln Leu Asp Tyr  
 425 430 435  
 Lys Asp Asp Asp Asp Lys  
 440

<210> 10  
 <211> 658  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> hSu(fu)-GST protein

<400> 10  
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln  
 1 5 10 15  
 Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu



	20	25	30
His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys	35	40	45
Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp	50	55	60
Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile	65	70	75
Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala	80	85	90
Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly	95	100	105
Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val	110	115	120
Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp	125	130	135
Arg Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His	140	145	150
Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met	155	160	165
Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys	170	175	180
Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser	185	190	195
Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe	200	205	210
Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg Gly	215	220	225
Ser Ala Glu Leu Arg Pro Ser Gly Ala Pro Gly Pro Thr Ala Pro	230	235	240
Pro Ala Pro Gly Pro Thr Ala Pro Pro Ala Phe Ala Ser Leu Phe	245	250	255
Pro Pro Gly Leu His Ala Ile Tyr Gly Glu Cys Arg Arg Leu Tyr	260	265	270
Pro Asp Gln Pro Asn Pro Leu Gln Val Thr Ala Ile Val Lys Tyr	275	280	285
Trp Leu Gly Gly Pro Asp Pro Leu Asp Tyr Val Ser Met Tyr Arg	290	295	300
Asn Val Gly Ser Pro Ser Ala Asn Ile Pro Glu His Trp His Tyr	305	310	315
Ile Ser Phe Gly Leu Ser Asp Leu Tyr Gly Asp Asn Arg Val His	320	325	330

Glu Phe Thr Gly Thr Asp Gly Pro Ser Gly Phe Gly Phe Glu Leu  
 335 340 345  
 Thr Phe Arg Leu Lys Arg Glu Thr Gly Glu Ser Ala Pro Pro Thr  
 350 355 360  
 Trp Pro Ala Glu Leu Met Gln Gly Leu Ala Arg Tyr Val Phe Gln  
 365 370 375  
 Ser Glu Asn Thr Phe Cys Ser Gly Asp His Val Ser Trp His Ser  
 380 385 390  
 Pro Leu Asp Asn Ser Glu Ser Arg Ile Gln His Met Leu Leu Thr  
 395 400 405  
 Glu Asp Pro Gln Met Gln Pro Val Gln Thr Pro Phe Gly Val Val  
 410 415 420  
 Thr Phe Leu Gln Ile Val Gly Val Cys Thr Glu Glu Leu His Ser  
 425 430 435  
 Ala Gln Gln Trp Asn Gly Gln Gly Ile Leu Glu Leu Leu Arg Thr  
 440 445 450  
 Val Pro Ile Ala Gly Gly Pro Trp Leu Ile Thr Asp Met Arg Arg  
 455 460 465  
 Gly Glu Thr Ile Phe Glu Ile Asp Pro His Leu Gln Glu Arg Val  
 470 475 480  
 Asp Lys Gly Ile Glu Thr Asp Gly Ser Asn Leu Ser Gly Val Ser  
 485 490 495  
 Ala Lys Cys Ala Trp Asp Asp Leu Ser Arg Pro Pro Glu Asp Asp  
 500 505 510  
 Glu Asp Ser Arg Ser Ile Cys Ile Gly Thr Gln Pro Arg Arg Leu  
 515 520 525  
 Ser Gly Lys Asp Thr Glu Gln Ile Arg Glu Thr Leu Arg Arg Gly  
 530 535 540  
 Leu Glu Ile Asn Ser Lys Pro Val Leu Pro Pro Ile Asn Pro Gln  
 545 550 555  
 Arg Gln Asn Gly Leu Ala His Asp Arg Ala Pro Ser Arg Lys Asp  
 560 565 570  
 Ser Leu Glu Ser Asp Ser Ser Thr Ala Ile Ile Pro His Glu Leu  
 575 580 585  
 Ile Arg Thr Arg Gln Leu Glu Ser Val His Leu Lys Phe Asn Gln  
 590 595 600  
 Glu Ser Gly Ala Leu Ile Pro Leu Cys Leu Arg Gly Arg Leu Leu  
 605 610 615  
 His Gly Arg His Phe Thr Tyr Lys Ser Ile Thr Gly Asp Met Ala  
 620 625 630

CR  
a  
Sub B

Ile Thr Phe Val Ser Thr Gly Val Glu Gly Ala Phe Ala Thr Glu  
635 640 645  
Glu His Pro Tyr Ala Ala His Gly Pro Trp Leu Gln Leu  
650 655